



## SEQUENCE LISTING

<110> Murphy, Anne N.  
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<120> COMPOSITIONS AND METHODS FOR DETERMINING  
INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR  
IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS

<130> 660088.433C1

<140> US 09/709,785

<141> 2000-11-03

<160> 57

<170> FastSEQ for Windows Version 3.0

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<211> 894

<212> DNA

<213> Homo sapien

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<210> 17  
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<400> 18  
aaatgataac catctcgc 18

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<400> 19  
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 <221> CDS  
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 ttg ggc cgc gtc tcc ttt gag ctg ttt gca gac aag gtc cca aag aca 96  
 Leu Gly Arg Val Ser Phe Glu Leu Phe Ala Asp Lys Val Pro Lys Thr  
 20 25 30  
 gca gaa aat ttt cgt gct ctg agc act gga gag aaa gga ttt ggt tat 144  
 Ala Glu Asn Phe Arg Ala Leu Ser Thr Gly Glu Lys Gly Phe Gly Tyr  
 35 40 45  
 aag ggt tcc tgc ttt cac aga att att cca ggg ttt atg tgt cag ggt 192  
 Lys Gly Ser Cys Phe His Arg Ile Ile Pro Gly Phe Met Cys Gln Gly  
 50 55 60  
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 Gly Asp Phe Thr Arg His Asn Gly Thr Gly Gly Lys Ser Ile Tyr Gly  
 65 70 75 80  
 gag aaa ttt gaa gat gag aac ttc atc cta aag cat acg ggt cct ggc 288  
 Glu Lys Phe Glu Asp Glu Asn Phe Ile Leu Lys His Thr Gly Pro Gly  
 85 90 95  
 atc ttg tcc atg gca aat gct gga ccc aac aca aat ggt tcc cag ttt 336  
 Ile Leu Ser Met Ala Asn Ala Gly Pro Asn Thr Asn Gly Ser Gln Phe  
 100 105 110  
 ttc atc tgc act gcc aag act gag tgg ttg gat ggc aag cat gtg gtg 384  
 Phe Ile Cys Thr Ala Lys Thr Glu Trp Leu Asp Gly Lys His Val Val  
 115 120 125  
 ttt ggc aaa gtg aaa gaa ggc atg aat att gtg gag gcc atg gag cgc 432  
 Phe Gly Lys Val Lys Glu Gly Met Asn Ile Val Glu Ala Met Glu Arg  
 130 135 140  
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Ala Glu Asn Phe Arg Ala Leu Ser Thr Gly Glu Lys Gly Phe Gly Tyr  
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 Lys Gly Ser Cys Phe His Arg Ile Ile Pro Gly Phe Met Cys Gln Gly  
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 Gly Asp Phe Thr Arg His Asn Gly Thr Gly Gly Lys Ser Ile Tyr Gly  
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 Glu Lys Phe Glu Asp Glu Asn Phe Ile Leu Lys His Thr Gly Pro Gly  
                   85                  90                  95  
 Ile Leu Ser Met Ala Asn Ala Gly Pro Asn Thr Asn Gly Ser Gln Phe  
                  100                 105                 110  
 Phe Ile Cys Thr Ala Lys Thr Glu Trp Leu Asp Gly Lys His Val Val  
                  115                 120                 125  
 Phe Gly Lys Val Lys Glu Gly Met Asn Ile Val Glu Ala Met Glu Arg  
                  130                 135                 140  
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 Cys Gly Gln Leu Glu  
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 <212> DNA  
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<220>  
 <223> PCR primer

<400> 28  
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42

<210> 29  
 <211> 42  
 <212> DNA  
 <213> Artificial Sequence

<220>  
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<400> 29  
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<210> 30  
 <211> 15  
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 <213> Artificial Sequence

<220>  
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 <211> 41  
 <212> DNA  
 <213> Artificial Sequence



<220>  
 <223> Primer for PCR amplification of human ANT3 for  
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<400> 31  
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<210> 32  
 <211> 42  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer for PCR amplification of human ANT3 for  
 expression constructs

<400> 32  
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<210> 33  
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 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer for PCR amplification of EYFP

<400> 33  
 gggcccctcg agatggtgag caagggcgag 30

<210> 34  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer for PCR amplification of EYFP

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<210> 35  
 <211> 34  
 <212> DNA  
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<220>  
 <223> PCR primer

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 <211> 35  
 <212> DNA  
 <213> Artificial Sequence

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&lt;223&gt; PCR Primer

&lt;400&gt; 36

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35

&lt;210&gt; 37

&lt;211&gt; 31

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; PCR Primer

&lt;400&gt; 37

ttaagatcc atggtcaacc ccaccgtgtt c

31

&lt;210&gt; 38

&lt;211&gt; 33

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; PCR primer

&lt;400&gt; 38

atatctcgag ttattcgagt tgtccacagt cag

33

&lt;210&gt; 39

&lt;211&gt; 624

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(621)

&lt;400&gt; 39

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ccg	cgc	tcc	gtg	ccg	ctg	cgc	ctc	ccc	gcg	gcc	cgc	gcc	tgc	agc	aag	96
Pro	Arg	Ser	Val	Pro	Leu	Arg	Leu	Pro	Ala	Ala	Arg	Ala	Cys	Ser	Lys	
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ggc	tcc	ggc	gac	ccg	tcc	tct	tcc	tcc	tcc	tcc	ggg	aac	ccg	ctc	gtg	144
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Tyr	Leu	Asp	Val	Asp	Ala	Asn	Gly	Lys	Pro	Leu	Gly	Arg	Val	Val	Leu	
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Leu Cys Thr Gly Glu Lys Gly Phe Gly Tyr Lys Gly Ser Thr Phe His	85	90	95	
agg gtg atc cct tcc ttc atg tgc cag gcg ggc gac ttc acc aac cac				336
Arg Val Ile Pro Ser Phe Met Cys Gln Ala Gly Asp Phe Thr Asn His	100	105	110	
aat ggc aca ggc ggg aag tcc atc tac gga agc cgc ttt cct gac gag				384
Asn Gly Thr Gly Gly Lys Ser Ile Tyr Gly Ser Arg Phe Pro Asp Glu	115	120	125	
aac ttt aca ctg aag cac gtg ggg cca ggt gtc ctg tcc atg gct aat				432
Asn Phe Thr Leu Lys His Val Gly Pro Gly Val Leu Ser Met Ala Asn	130	135	140	
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Ala Gly Pro Asn Thr Asn Gly Ser Gln Phe Phe Ile Cys Thr Ile Lys	145	150	155	160
aca gac tgg ttg gat ggc aag cat gtt gtg ttc ggt cac gtc aaa gag				528
Thr Asp Trp Leu Asp Gly Lys His Val Val Phe Gly His Val Lys Glu	165	170	175	
ggc atg gac gtc gtg aag aaa ata gaa tct ttc ggc tct aag agt ggg				576
Gly Met Asp Val Val Lys Lys Ile Glu Ser Phe Gly Ser Lys Ser Gly	180	185	190	
agg aca tcc aag aag att gtc atc aca gac tgt ggc cag ttg agc				621
Arg Thr Ser Lys Lys Ile Val Ile Thr Asp Cys Gly Gln Leu Ser	195	200	205	
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<212> PRT				
<213> Homo sapien				

<400> 40															
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			20					25					30		
Gly	Ser	Gly	Asp	Pro	Ser	Ser	Ser	Ser	Ser	Gly	Asn	Pro	Leu	Val	
		35				40					45				
Tyr	Leu	Asp	Val	Asp	Ala	Asn	Gly	Lys	Pro	Leu	Gly	Arg	Val	Val	Leu
	50				55					60					
Glu	Leu	Lys	Ala	Asp	Val	Val	Pro	Lys	Thr	Ala	Glu	Asn	Phe	Arg	Ala
65				70					75					80	
Leu	Cys	Thr	Gly	Glu	Lys	Gly	Phe	Gly	Tyr	Lys	Gly	Ser	Thr	Phe	His
			85					90						95	
Arg	Val	Ile	Pro	Ser	Phe	Met	Cys	Gln	Ala	Gly	Asp	Phe	Thr	Asn	His
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Asn	Phe	Thr	Leu	Lys	His	Val	Gly	Pro	Gly	Val	Leu	Ser	Met	Ala	Asn
Ala	Gly	Pro	Asn	Thr	Asn	Gly	Ser	Gln	Phe	Phe	Ile	Cys	Thr	Ile	Lys
Thr	Asp	Trp	Leu	Asp	Gly	Lys	His	Val	Val	Phe	Gly	His	Val	Lys	Glu
Gly	Met	Asp	Val	Val	Lys	Lys	Ile	Glu	Ser	Phe	Gly	Ser	Lys	Ser	Gly
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<211> 31
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<213> Artificial Sequence
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<210> 42
<211> 32
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<213> Artificial Sequence
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<213> Artificial Sequence
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<220>  
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<210> 45

<211> 36  
 <212> DNA  
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32

<210> 47  
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 <212> PRT  
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 35 40 45  
 Lys Gln Tyr Lys Gly Ile Ile Asp Cys Val Val Arg Ile Pro Lys Glu  
 50 55 60  
 Gln Gly Phe Leu Ser Phe Trp Arg Gly Asn Leu Ala Asn Val Ile Arg  
 65 70 75 80  
 Tyr Phe Pro Thr Gln Ala Leu Asn Phe Ala Phe Lys Asp Lys Tyr Lys  
 85 90 95  
 Gln Leu Phe Leu Gly Gly Val Asp Arg His Lys Gln Phe Trp Arg Tyr  
 100 105 110  
 Phe Ala Gly Asn Leu Ala Ser Gly Gly Ala Ala Gly Ala Thr Ser Leu  
 115 120 125  
 Cys Phe Val Tyr Pro Leu Asp Phe Ala Arg Thr Arg Leu Ala Ala Asp  
 130 135 140  
 Val Gly Arg Arg Ala Gln Arg Glu Phe His Gly Leu Gly Asp Cys Ile  
 145 150 155 160  
 Ile Lys Ile Phe Lys Ser Asp Gly Leu Arg Gly Leu Tyr Gln Gly Phe  
 165 170 175  
 Asn Val Ser Val Gln Gly Ile Ile Ile Tyr Arg Ala Ala Tyr Phe Gly  
 180 185 190  
 Val Tyr Asp Thr Ala Lys Gly Met Leu Pro Asp Pro Lys Asn Val His  
 195 200 205  
 Ile Phe Val Ser Trp Met Ile Ala Gln Ser Val Thr Ala Val Ala Gly  
 210 215 220  
 Leu Leu Ser Tyr Pro Phe Asp Thr Val Arg Arg Arg Met Met Met Gln  
 225 230 235 240

Ser	Gly	Arg	Lys	Gly	Ala	Asp	Ile	Met	Tyr	Thr	Gly	Thr	Val	Asp	Cys
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Trp	Arg	Lys	Ile	Ala	Lys	Asp	Glu	Gly	Ala	Lys	Ala	Phe	Phe	Lys	Gly
			260					265					270		
Ala	Trp	Ser	Asn	Val	Leu	Arg	Gly	Met	Gly	Gly	Ala	Phe	Val	Leu	Val
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	290					295									

<210> 48  
 <211> 298  
 <212> PRT  
 <213> Homo sapien

<400> 48															
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			20					25					30		
Lys	Leu	Leu	Leu	Gln	Val	Gln	His	Ala	Ser	Lys	Gln	Ile	Thr	Ala	Asp
		35				40						45			
Lys	Gln	Tyr	Lys	Gly	Ile	Ile	Asp	Cys	Val	Val	Arg	Ile	Pro	Lys	Glu
	50					55					60				
Gln	Glu	Val	Leu	Ser	Phe	Trp	Arg	Gly	Asn	Leu	Ala	Asn	Val	Ile	Arg
65					70				75						80
Tyr	Phe	Pro	Thr	Gln	Ala	Leu	Asn	Phe	Ala	Phe	Lys	Asp	Lys	Tyr	Lys
				85				90						95	
Gln	Ile	Phe	Leu	Gly	Gly	Val	Asp	Lys	Arg	Thr	Gln	Phe	Trp	Arg	Tyr
			100					105					110		
Phe	Ala	Gly	Asn	Leu	Ala	Ser	Gly	Gly	Ala	Ala	Gly	Ala	Thr	Ser	Leu
		115					120					125			
Cys	Phe	Val	Tyr	Pro	Leu	Asp	Phe	Ala	Arg	Thr	Arg	Leu	Ala	Ala	Asp
		130				135					140				
Val	Gly	Lys	Ala	Gly	Ala	Glu	Arg	Glu	Phe	Arg	Gly	Leu	Gly	Asp	Cys
145					150				155						160
Leu	Val	Lys	Ile	Tyr	Lys	Ser	Asp	Gly	Ile	Lys	Gly	Leu	Tyr	Gln	Gly
			165					170						175	
Phe	Asn	Val	Ser	Val	Gln	Gly	Ile	Ile	Ile	Tyr	Arg	Ala	Ala	Tyr	Phe
			180				185						190		
Gly	Ile	Tyr	Asp	Thr	Ala	Lys	Gly	Met	Leu	Pro	Asp	Pro	Lys	Asn	Thr
		195					200					205			
His	Ile	Val	Ile	Ser	Trp	Met	Ile	Ala	Gln	Thr	Val	Thr	Ala	Val	Ala
	210					215					220				
Gly	Leu	Thr	Ser	Tyr	Pro	Phe	Asp	Thr	Val	Arg	Arg	Arg	Met	Met	Met
225					230					235					240
Gln	Ser	Gly	Arg	Lys	Gly	Thr	Asp	Ile	Met	Tyr	Thr	Gly	Thr	Leu	Asp
				245					250					255	
Cys	Trp	Arg	Lys	Ile	Ala	Arg	Asp	Glu	Gly	Gly	Lys	Ala	Phe	Phe	Lys
			260					265					270		
Gly	Ala	Trp	Ser	Asn	Val	Leu	Arg	Gly	Met	Gly	Gly	Ala	Phe	Val	Leu
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Val	Leu	Tyr	Asp	Glu	Ile	Lys	Lys	Tyr	Thr						
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<210> 49  
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 <212> PRT

&lt;213&gt; Homo sapien

&lt;400&gt; 49

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Lys Leu Leu Leu Gln Val Gln His Ala Ser Lys Gln Ile Ala Ala Asp
          35          40          45
Lys Gln Tyr Lys Gly Ile Val Asp Cys Ile Val Arg Ile Pro Lys Glu
          50          55          60
Gln Gly Val Leu Ser Phe Trp Arg Gly Asn Leu Ala Asn Val Ile Arg
65          70          75          80
Tyr Phe Pro Thr Gln Ala Leu Asn Phe Ala Phe Lys Asp Lys Tyr Lys
          85          90          95
Gln Ile Phe Leu Gly Gly Val Asp Lys His Thr Gln Phe Trp Arg Tyr
          100          105          110
Phe Ala Gly Asn Leu Ala Ser Gly Gly Ala Ala Gly Ala Thr Ser Leu
          115          120          125
Cys Phe Val Tyr Pro Leu Asp Phe Ala Arg Thr Arg Leu Ala Ala Asp
          130          135          140
Val Gly Lys Ser Gly Thr Glu Arg Glu Phe Arg Gly Leu Gly Asp Cys
145          150          155          160
Leu Val Lys Ile Thr Lys Ser Asp Gly Ile Arg Gly Leu Tyr Gln Gly
          165          170          175
Phe Ser Val Ser Val Gln Gly Ile Ile Ile Tyr Arg Ala Ala Tyr Phe
          180          185          190
Gly Val Tyr Asp Thr Ala Lys Gly Met Leu Pro Asp Pro Lys Asn Thr
          195          200          205
His Ile Val Val Ser Trp Met Ile Ala Gln Thr Val Thr Ala Val Ala
          210          215          220
Gly Val Val Ser Tyr Pro Phe Asp Thr Val Arg Arg Arg Met Met Met
225          230          235          240
Gln Ser Gly Arg Lys Gly Ala Asp Ile Met Tyr Thr Gly Thr Val Asp
          245          250          255
Cys Trp Arg Lys Ile Phe Arg Asp Glu Gly Gly Lys Ala Phe Phe Lys
          260          265          270
Gly Ala Trp Ser Asn Val Leu Arg Gly Met Gly Gly Ala Phe Val Leu
          275          280          285
Val Leu Tyr Asp Glu Leu Lys Lys Val Ile
          290          295

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&lt;210&gt; 50

&lt;211&gt; 4

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Synthetic peptide

&lt;400&gt; 50

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Tyr Val Ala Asp
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&lt;210&gt; 51

&lt;211&gt; 5

&lt;212&gt; PRT

<213> Homo sapien

<400> 51

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<212> PRT

<213> Homo sapien

<400> 52

Gly Ser Pro Gly Ile Leu  
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<210> 53

<211> 4

<212> PRT

<213> Homo sapien

<400> 53

Pro Ser Ser Ser  
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<210> 54

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<212> PRT

<213> Homo sapien

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<210> 55

<211> 8

<212> PRT

<213> Artificial Sequence

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<223> Epitope tag

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<210> 56

<211> 8

<212> PRT

<213> Artificial Sequence

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<223> Epitope tag

<400> 56

Asp Leu Tyr Asp Asp Asp Asp Lys  
1 5



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C/

<400> 57

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ggcatgggtg	gtgcttttgt	gcttgtcttg	tatgatgaaa	tcaagaagta	cacataa	897

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